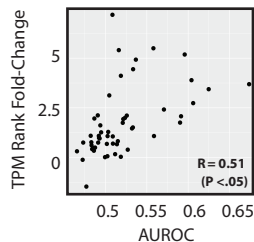


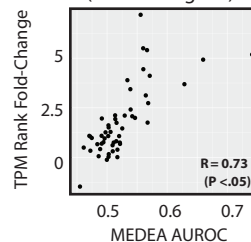
AUROC with GENRE

MEDEA

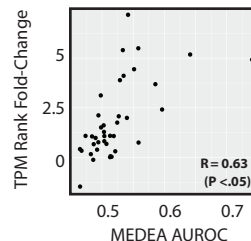
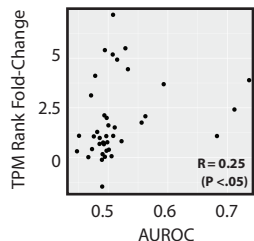
ATAC-seq data



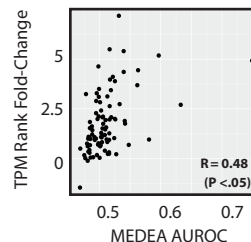
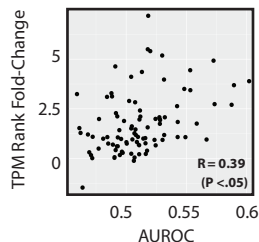
(Same as Fig. 6C)



scATAC-seq data



FAIRE-seq data



Supplemental Figure S15

Supplemental Figure S15: RNA-seq validation of motif enrichment patterns vary based on background set and motif enrichment tool. For each heatmap in **Fig. 6A-B**, the scatterplots comparing the motif enrichment values denoted in the heatmaps and the corresponding TFs' RNA-seq up-regulation (TPM Rank Fold-Change values from **Fig. 1B**). As noted, the scatter plot for MEDEA in ATAC-seq data (top-right panel) is the same as in **Fig. 6C**. Pearson's R values are compared in **Fig. 6D**.